

PubMed	Nucleotide	Protein	Genome	Structure	PopSet	Taxonomy	OMIM	
Search	Protein	▼ for					Go	Clear
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Display	Default View	▼ as	HTML	▼	Save	Add to Clipboard		

☐ 1: **P54926 MYO-INOSITOL-1(OR 4)-MONOPHOSPHATASE 1 (IMPASE 1) (IMP 1) (INOSITOL MONOPHOSPHATASE 1)** BLink, PubMed, Related Sequences, Taxonomy

LOCUS MYO1_LYCES 273 aa PLN 01-OCT-2000
DEFINITION MYO-INOSITOL-1(OR 4)-MONOPHOSPHATASE 1 (IMPASE 1) (IMP 1) (INOSITOL MONOPHOSPHATASE 1).
ACCESSION P54926
PID g1709203
VERSION P54926 GI:1709203
DBSOURCE swissprot: locus MYO1_LYCES, accession P54926;
class: standard.
created: Oct 1, 1996.
sequence updated: Oct 1, 1996.
annotation updated: Oct 1, 2000.
xrefs: gi: gi: 1098976, gi: gi: 1098977
xrefs (non-sequence databases): HSSP P29218, InterPro IPR000760,
Pfam PF00459, PRINTS PR00378, PROSITE PS00629, PROSITE PS00630
KEYWORDS Hydrolase; Magnesium; Lithium; Multigene family.
SOURCE tomato.
ORGANISM *Lycopersicon esculentum*
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids
I; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE 1 (residues 1 to 273)
AUTHORS Gillasp, G.E., Keddle, J.S., Oda, K. and Gruissem, W.
TITLE Plant inositol monophosphatase is a lithium-sensitive enzyme
encoded by a multigene family
JOURNAL Plant Cell 7 (12), 2175-2185 (1995)
MEDLINE 96351935
REMARK SEQUENCE FROM N.A.
STRAIN=CV. VFNT CHERRY

COMMENT

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collaboration between the Swiss Institute of Bioinformatics and
the EMBL outstation - the European Bioinformatics Institute.
The original entry is available from <http://www.expasy.ch/sprot>
and <http://www.ebi.ac.uk/sprot>

[FUNCTION] IT IS RESPONSIBLE FOR THE PROVISION OF INOSITOL REQUIRED
FOR SYNTHESIS OF PHOSPHATIDYLINOSITOL AND POLYPHOSPHOINOSITIDES.
[CATALYTIC ACTIVITY] MYO-INOSITOL 1-MONOPHOSPHATE + H(2)O =
MYO-INOSITOL + ORTHOPHOSPHATE.
[COFACTOR] REQUIRES MAGNESIUM (BY SIMILARITY).
[ENZYME REGULATION] INHIBITED BY LI(+).
[PATHWAY] KEY ENZYME OF THE PHOSPHATIDYL INOSITOL SIGNALING
PATHWAY.
[SIMILARITY] BELONGS TO THE INOSITOL MONOPHOSPHATASE FAMILY.

FEATURES

source

Location/Qualifiers

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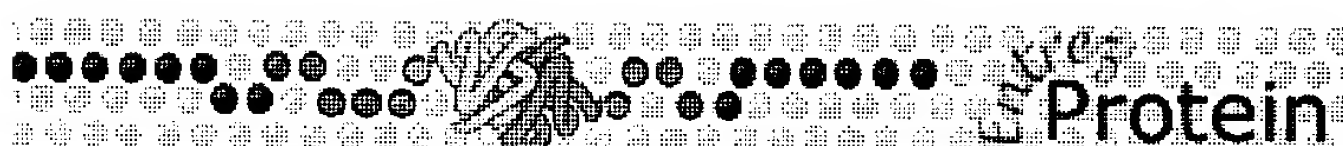
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/product="MYO-INOSITOL-1(OR 4)-MONOPHOSPHATASE 1"
/EC_number="3.1.3.25"

ORIGIN

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181 nllfkvrsl rmcgscaldl cwwacgrlel fyligyggpw dvaggavivk eaggvlfdps
241 gsefditsqr vaatnphlke afvealqlse yvs


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PubMed	Nucleotide	Protein	Genome	Structure	PopSet	Taxonomy	OMIM	
Search	Protein	for					Go	Clear
Limits		Index	History	Clipboard				
Display	Default View	as	HTML	Save	Add to Clipboard			

☐ 1: P74158 **EXTRAGENIC SUPPRESSOR** BLink, PubMed, Related Sequences, Taxonomy
PROTEIN SUHB HOMOLOG

LOCUS SUHB_SYNY3 287 aa .BCT 15-DEC-1998
DEFINITION EXTRAGENIC SUPPRESSOR PROTEIN SUHB HOMOLOG. 
ACCESSION P74158
PID g3915048
VERSION P74158 GI:3915048
DBSOURCE swissprot: locus SUHB_SYNY3, accession P74158;
class: standard.
created: Dec 15, 1998.
sequence updated: Dec 15, 1998.
annotation updated: Dec 15, 1998.
xrefs: gi: gi: 1653228, gi: gi: 1653332
xrefs (non-sequence databases): PFAM PF00459, PROSITE PS00629,
PROSITE PS00630
KEYWORDS .
SOURCE Synechocystis PCC6803.
ORGANISM Synechocystis PCC6803
Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
REFERENCE 1 (residues 1 to 287)
AUTHORS KANEKO,T., SATO,S., KOTANI,H., TANAKA,A., ASAMIZU,E., NAKAMURA,Y.,
MIYAJIMA,N., HIROSAWA,M., SUGIURA,M., SASAMOTO,S., KIMURA,T.,
HOSOUCHI,T., MATSUNO,A., MURAKI,A., NAKAZAKI,N., NARUO,K.,
OKUMURA,S., SHIMPO,S., TAKEUCHI,C., WADA,T., WATANABE,A.,
YAMADA,M., YASUDA,M. and TABATA,S.
TITLE Sequence analysis of the genome of the unicellular cyanobacterium
Synechocystis sp. strain PCC6803. II. Sequence determination of the
entire genome and assignment of potential protein-coding regions
JOURNAL DNA Res. 3 (3), 109-136 (1996)
MEDLINE 97061201
REMARK SEQUENCE FROM N.A.
COMMENT

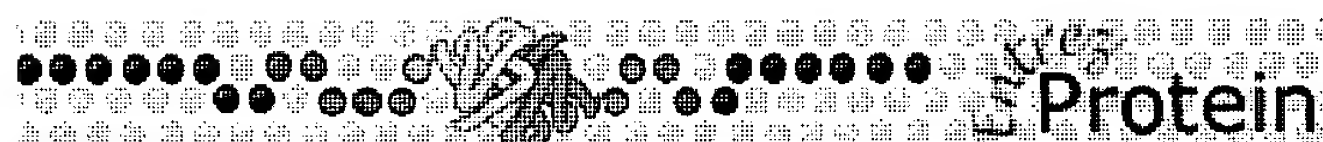
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collaboration between the Swiss Institute of Bioinformatics and
the EMBL outstation - the European Bioinformatics Institute.
The original entry is available from <http://www.expasy.ch/sprot>
and <http://www.ebi.ac.uk/sprot>

[SIMILARITY] BELONGS TO THE INOSITOL MONOPHOSPHATASE FAMILY.
FEATURES Location/Qualifiers
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/db_xref="taxon:1148"
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Protein 1..287
/product="EXTRAGENIC SUPPRESSOR PROTEIN SUHB HOMOLOG"

ORIGIN

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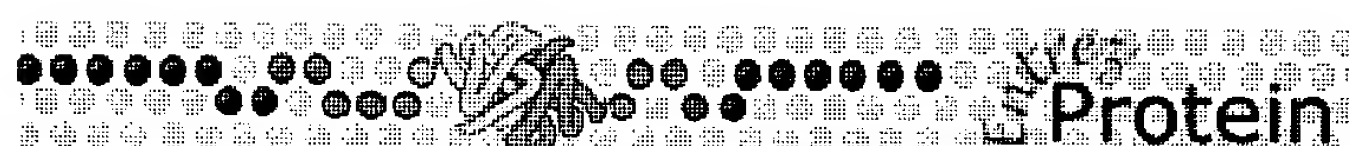
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PubMed	Nucleotide	Protein	Genome	Structure	PopSet	Taxonomy	OMIM
Search	Protein	▼ for					Go Clear
Limits		Index	History	Clipboard			
Display	Default View	▼ as	HTML	▼ Save	Add to Clipboard		

☐ 1: BAA17860 **extragenic** BLink, PubMed, Related Sequences, Nucleotide, Genome, Ta
suppressor
[Synechocystis
sp.]

LOCUS BAA17860 267 aa BCT 07-FEB-1999
 DEFINITION extragenic suppressor [Synechocystis sp.].
 ACCESSION BAA17860
 PID g1652942
 VERSION BAA17860.1 GI:1652942
 DBSOURCE locus D90909 accession D90909.1
 KEYWORDS .
 SOURCE Synechocystis sp.
 ORGANISM Synechocystis sp.
 Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
 REFERENCE 1 (sites)
 AUTHORS Kaneko,T., Sato,S., Kotani,H., Tanaka,A., Asamizu,E., Nakamura,Y.,
 Miyajima,N., Hirose,M., Sugiura,M., Sasamoto,S., Kimura,T.,
 Hosouchi,T., Matsuno,A., Muraki,A., Nakazaki,N., Naruo,K.,
 Okumura,S., Shimpo,S., Takeuchi,C., Wada,T., Watanabe,A.,
 Yamada,M., Yasuda,M. and Tabata,S.
 TITLE Sequence analysis of the genome of the unicellular cyanobacterium
 Synechocystis sp. strain PCC6803. II. Sequence determination of the
 entire genome and assignment of potential protein-coding regions
 JOURNAL DNA Res. 3 (3), 109-136 (1996)
 MEDLINE 97061201
 REFERENCE 2 (residues 1 to 267)
 AUTHORS Tabata,S.
 TITLE Direct Submission
 JOURNAL Submitted (28-JUN-1996) Satoshi Tabata, Kazusa DNA Research
 Institute, Laboratory of Gene Structure 2; 1523-3, Yanauchino,
 Kisarazu, Chiba 292, Japan (E-mail:tabata@kazusa.or.jp,
 Tel:+81-438-52-3933, Fax:+81-438-52-3934)
 COMMENT Potential protein coding regions were assigned on the basis of
 similarity search of the ORFs and GeneMark analysis.
 FEATURES Location/Qualifiers
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 /organism="Synechocystis sp."
 /strain="PCC6803"
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 Protein 1..267
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 /note="ORF_ID:s111959"
 ORIGIN
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 61 qaqfpqdgvi reegkniagk sgytwvldpi dgtssfvrgl pifatliglv dadmrpvlgi
 121 ahqpisgdrw qgvqgeqsnv ngiplvnpyk aseintltaac ivsttplmft tpvqqqkmad
 181 iyrqcqrtaf ggdcfnylsa asgwtamplv iveadlnfyd fcalipiltg anycftdwqg
 241 keltpestev vaspnpklhs eilaflq
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PubMed	Nucleotide	Protein	Genome	Structure	PopSet	Taxonomy	OMIM	
Search	Protein	for					Go	Clear
Limits		Index	History	Clipboard				
Display	Default View	as	HTML	Save	Add to Clipboard			

☐ 1: **P54928 MYO-INOSITOL-1(OR 4)-MONOPHOSPHATASE 3 (IMPASE 3) (IMP 3) (INOSITOL MONOPHOSPHATASE 3)** BLink, PubMed, Related Sequences, Taxonomy

LOCUS MYO3_LYCES 268 aa PLN 01-OCT-2000
DEFINITION MYO-INOSITOL-1(OR 4)-MONOPHOSPHATASE 3 (IMPASE 3) (IMP 3) (INOSITOL MONOPHOSPHATASE 3).
ACCESSION P54928
PID g1709205
VERSION P54928 GI:1709205
DBSOURCE swissprot: locus MYO3_LYCES, accession P54928;
class: standard.
created: Oct 1, 1996.
sequence updated: Oct 1, 1996.
annotation updated: Oct 1, 2000.
xrefs: gi: gi: 1098970, gi: gi: 1098971
xrefs (non-sequence databases): HSSP P29218, InterPro IPR000760, Pfam PF00459, PRINTS PR00378, PROSITE PS00629, PROSITE PS00630
KEYWORDS Hydrolase; Magnesium; Lithium; Multigene family.
SOURCE tomato.
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE 1 (residues 1 to 268)
AUTHORS Gillasp, G.E., Keddle, J.S., Oda, K. and Gruissem, W.
TITLE Plant inositol monophosphatase is a lithium-sensitive enzyme encoded by a multigene family
JOURNAL Plant Cell 7 (12), 2175-2185 (1995)
MEDLINE 96351935
REMARK SEQUENCE FROM N.A.
STRAIN=CV. VFNT CHERRY

COMMENT

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[FUNCTION] IT IS RESPONSIBLE FOR THE PROVISION OF INOSITOL REQUIRED FOR SYNTHESIS OF PHOSPHATIDYLINOSITOL AND POLYPHOSPHOINOSITIDES.

[CATALYTIC ACTIVITY] MYO-INOSITOL 1-MONOPHOSPHATE + H(2)O = MYO-INOSITOL + ORTHOPHOSPHATE.

[COFACTOR] REQUIRES MAGNESIUM (BY SIMILARITY).

[ENZYME REGULATION] INHIBITED BY LI(+).

[PATHWAY] KEY ENZYME OF THE PHOSPHATIDYL INOSITOL SIGNALING PATHWAY.

[SIMILARITY] BELONGS TO THE INOSITOL MONOPHOSPHATASE FAMILY.

FEATURES

source

Location/Qualifiers

1..268

/organism="Lycopersicon esculentum"

Protein /db_xref="taxon:4081"
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 /product="MYO-INOSITOL-1 (OR 4) -MONOPHOSPHATASE 3"
 /EC_number="3.1.3.25"

ORIGIN

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121  gvvynpiide lftgidgkga flngkpikvs sqselvkall ateagtnrdk lvvdattgri
181  nsllfkvrsl rmcgscalnl cgvacgrldl fyelefggpw dvaggavivk eaggfvfdps
241  gsefdltarr vaatnahlkd afikalne
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